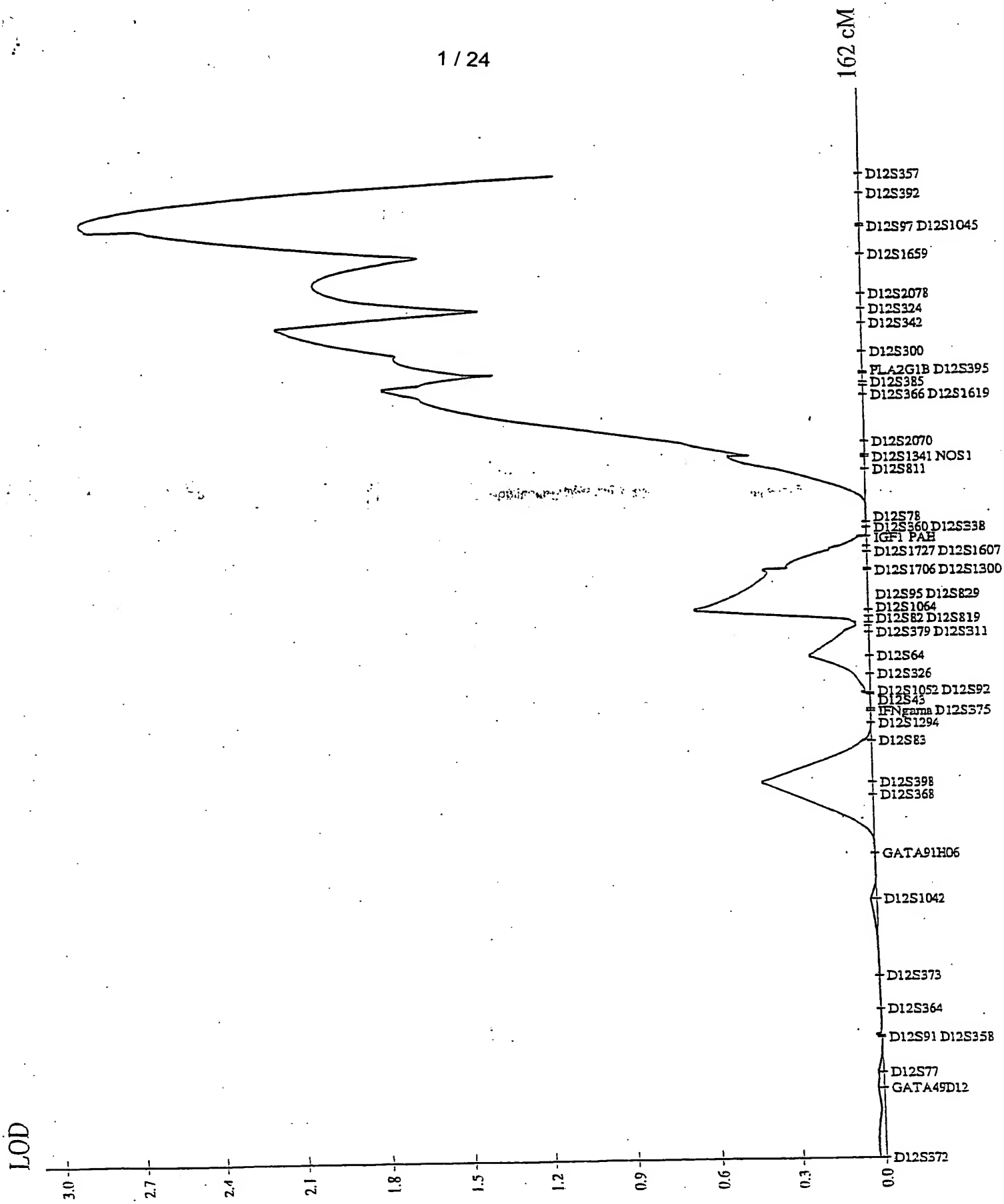
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D12S360 D12S338
IGF1 PAH
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D12S1064
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D12S64
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D12S43
IFNgamma D12S375
D12S1294
D12S83
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D12S364
D12S91 D12S358
D12S77
GATA49D12
D12S372
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2.7
2.4
2.1
1.8
1.5
1.2
0.9
0.6
0.3
0.0

Figure 1

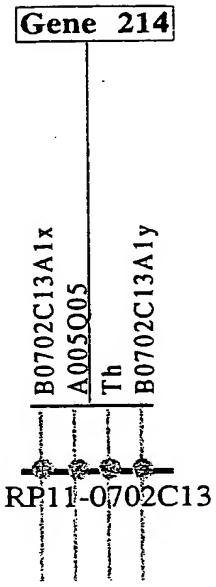


Figure 2

```
        10                  30                  50
        .                   .                   .                   .
TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG
  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  V

        70                  90                  110
        .                   .                   .                   .
TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG
  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E  R  T  R  V

        130                 150                 170
        .                   .                   .                   .
TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC
  H  E  L  A  T  S  S  A  G  R  D  P  G  S  T  S  C  P  R  P

        190                 210                 230
        .                   .                   .                   .
CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCC
  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  K  G  P  R

        250                 270                 290
        .                   .                   .                   .
GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC
  V  H  E  L  P  T  S  S  P  G  R  D  P  G  S  T  N  C  P  R

        310                 330                 350
        .                   .                   .                   .
GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC
  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  R  G  H

        370                 390                 410
        .                   .                   .                   .
ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC
  R  V  H  E  L  P  T  P  S  P  G  R  D  P  G  F  M  S  C  P

        430                 450                 470
        .                   .                   .                   .
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG
  R  P  L  Q  E  G  T  R  V  H  E  L  P  T  P  S  P  G  G  D

        490                 510                 530
        .                   .                   .                   .
ACCCGGGTCCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCGGGTCCACGAGCTGCC
  P  G  P  R  A  A  H  V  V  N  G  K  G  P  G  S  T  S  C  P
```

Figure 3A

```
      550                 570                 590
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG
  R  P  L  Q  E  G  T  R  V  H  E  L  P  T  R  S  P  G  G  D

      610                 630                 650
ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG
  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A

      670                 690                 710
CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG
  H  V  L  S  R  R  G  H  R  V  H  E  L  P  T  S  S  P  G  G

      730                 750                 770
GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG
  D  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A

      790                 810                 830
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
  A  H  V  L  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E

      850                 870                 890
AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG
  G  T  P  G  S  R  A  A  H  A  L  S  R  K  G  P  R  V  Q  V

      910                 930                 950
TCTCCTGCCGGCCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCCC
  S  C  R  P  T  S  C  L  C  V  N  Q  K  K  D  E  E  Q  A  L

      970                 990                 1010
TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG
  L  S  L  Q  A  G  F  G  G  G  A  G  S  P  A  A  P  S  L  A

      1030                1050                1070
CAGGGCACCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA
  G  H  P  V  L  E  P  Q  N  C  R  R  P  A  E  K  G  S  M  M
```

Figure 3B

```
      1090                1110                1130
TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCCATGGACCTGGGAACCTCCCGGCTCTT
  A  P  R  C  A  A  L  D  L  P  P  W  T  W  E  P  P  G  S  S

      1150                1170                1190
CCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGGTCGGCCAGGCCCCATCCCCGTACCCT
  H  S  G  K  E  G  S  G  H  G  G  R  P  G  P  I  P  V  P  W

      1210                1230                1250
GGCCCTTCTTCCTGCTTCCTGTTTGTCACTGCCCCGGGGCCTTTGCACCTGCATTCCCTC
  P  F  F  L  L  P  V  C  H  C  P  G  A  F  A  P  A  F  P  L

      1270                1290                1310
TCTCTAGACAGGGTTTCTCCTCATTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGACGA
  S  R  Q  G  F  S  S  L  A  R  L  V  S  N  S  *

      1330                1350                1370
TCCACCTGCCTCAGCCTCCCGAAGTGTTGGGATTACAGGCACGAGCCACTGTGCCCGGCC

      1390                1410                1430
ATCATTCCTTTTTACTGCTGACTAATAGTCTGCTGTGTGAATCCACCGCTAGAAACCCAC

      1450                1470                1490
TCATCAGTTGATGGTCATGTGGGTTGCTTCTGCTATTCGCTTATTATGAACAGTGCTGGA

      1510                1530                1550
ATAAACGTTCCTGTGCACTCTTGGGCATACGCCTAGGAGTGGAACTGCTGGGTCAAAAAA

      1570
AAAAAAAAAAAAAAAAAAAA
```

Figure 3C

```
        10                  30                  50
TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG
  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  V

        70                  90                  110
TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG
  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E  R  T  R  V

        130                 150                 170
TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC
  H  E  L  A  T  S  S  A  G  R  D  P  G  S  T  S  C  P  R  P

        190                 210                 230
CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCC
  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  K  G  P  R

        250                 270                 290
GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC
  V  H  E  L  P  T  S  S  P  G  R  D  P  G  S  T  N  C  P  R

        310                 330                 350
GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC
  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  R  G  H

        370                 390                 410
ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC
  R  V  H  E  L  P  T  P  S  P  G  R  D  P  G  F  M  S  C  P

        430                 450                 470
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG
  R  P  L  Q  E  G  T  R  V  H  E  L  P  T  P  S  P  G  G  D

        490                 510                 530
ACCCGGGTCCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCGGGTCCACGAGCTGCC
  P  G  P  R  A  A  H  V  V  N  G  K  G  P  G  S  T  S  C  P

        550                 570                 590
```

Figure 4A

```
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG
  R  P  L  Q  E  G  T  R  V  H  E  L  P  T  R  S  P  G  G  D

       610                 630                 650
ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG
  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A

       670                 690                 710
CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG
  H  V  L  S  R  R  G  H  R  V  H  E  L  P  T  S  S  P  G  G

       730                 750                 770
GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG
  D  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A

       790                 810                 830
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
  A  H  V  L  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E

       850                 870                 890
AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG
  G  T  P  G  S  R  A  A  H  A  L  S  R  K  G  P  R  V  Q  V

       910                 930                 950
TCTCCTGCCGGCCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCCC
  S  C  R  P  T  S  C  L  C  V  N  Q  K  K  D  E  E  Q  A  L

       970                 990                 1010
TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG
  L  S  L  Q  A  G  F  G  G  G  A  G  S  P  A  A  P  S  L  A

       1030                1050                1070
CAGGGCACCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA
  G  H  P  V  L  E  P  Q  N  C  R  R  P  A  E  K  G  S  M  M

       1090                1110                1130
TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCCATGGACCTGGAGACAGGGTTTCTCCT
  A  P  R  C  A  A  L  D  L  P  P  W  T  W  R  Q  G  F  S  S
```

Figure 4B

```
      1150                1170                1190
        .                   .                   .
CATTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGACGATCCACCTGCCTCAGCCTCCCG
  L  A  R  L  V  S  N  S  *

      1210                1230                1250
        .                   .                   .
AAGTGTTGGGATTACAGGCACGAGCCACTGTGCCCGGCCATCATTCCTTTTTACTGCTGA

      1270                1290                1310
        .                   .                   .
CTAATAGTCTGCTGTGTGAATCCACCGCTAGAAACCCACTCATCAGTTGATGGTCATGTG

      1330                1350                1370
        .                   .                   .
GGTTGCTTCTGCTATTCGCTTATTATGAACAGTGCTGGAATAAACGTTCCTGTGCACTCT

      1390                1410                1430
        .                   .                   .
TGGGCATACGCCTAGGAGTGGAACTGCTGGGTCAAAAAAAAAAAAAAAAAAAAAAAAAA
```

A

Figure 4C

```
          10                  30                  50
TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG
  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  V

          70                  90                 110
TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG
  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E  R  T  R  V

         130                 150                 170
TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC
  H  E  L  A  T  S  S  A  G  R  D  P  G  S  T  S  C  P  R  P

         190                 210                 230
CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCC
  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  K  G  P  R

         250                 270                 290
GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC
  V  H  E  L  P  T  S  S  P  G  R  D  P  G  S  T  N  C  P  R

         310                 330                 350
GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC
  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  R  G  H

         370                 390                 410
ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC
  R  V  H  E  L  P  T  P  S  P  G  R  D  P  G  F  M  S  C  P

         430                 450                 470
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG
  R  P  L  Q  E  G  T  R  V  H  E  L  P  T  P  S  P  G  G  D

         490                 510                 530
ACCCGGGTCCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCGGGTCCACGAGCTGCC
  P  G  P  R  A  A  H  V  V  N  G  K  G  P  G  S  T  S  C  P
```

Figure 5A

```
      550                 570                 590
       .                   .                   .                   .
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG
  R  P  L  Q  E  G  T  R  V  H  E  L  P  T  R  S  P  G  G  D

      610                 630                 650
       .                   .                   .                   .
ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG
  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A

      670                 690                 710
       .                   .                   .                   .
CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG
  H  V  L  S  R  R  G  H  R  V  H  E  L  P  T  S  S  P  G  G

      730                 750                 770
       .                   .                   .                   .
GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG
  D  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A

      790                 810                 830
       .                   .                   .                   .
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
  A  H  V  L  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E

      850                 870                 890
       .                   .                   .                   .
AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG
  G  T  P  G  S  R  A  A  H  A  L  S  R  K  G  P  R  V  Q  V

      910                 930                 950
       .                   .                   .                   .
TCTCCTGCCGGCCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCCC
  S  C  R  P  T  S  C  L  C  V  N  Q  K  K  D  E  E  Q  A  L

      970                 990                 1010
       .                   .                   .                   .
TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG
  L  S  L  Q  A  G  F  G  G  G  A  G  S  P  A  A  P  S  L  A

      1030                1050                1070
       .                   .                   .                   .
CAGGGCACCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA
  G  H  P  V  L  E  P  Q  N  C  R  R  P  A  E  K  G  S  M  M
```

Figure 5B

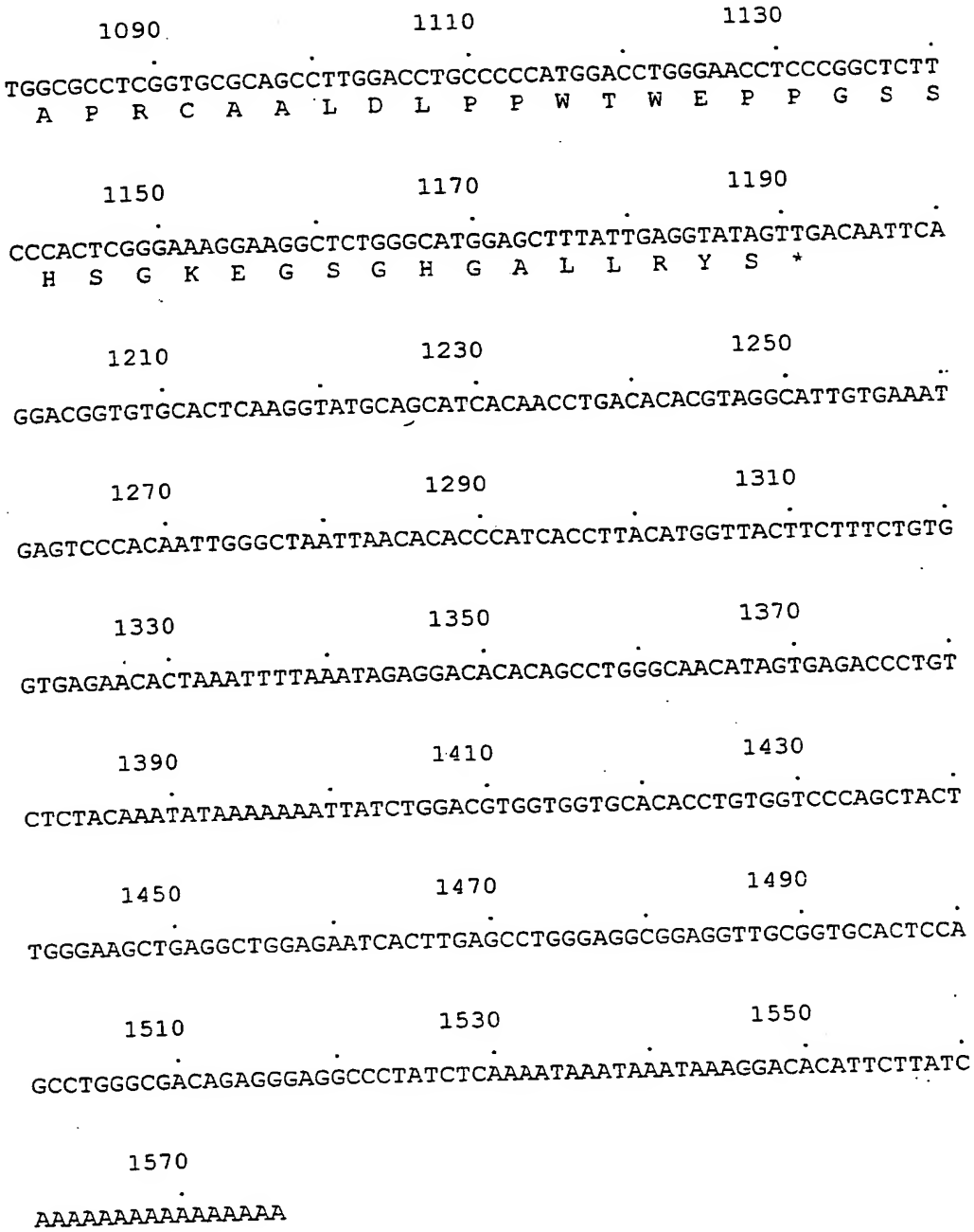

1090
1110
1130
TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCCATGGACCTGGGAACCTCCCGGCTCTT
A P R C A A L D L P P W T W E P P G S S
1150
1170
1190
CCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGCTTTATTGAGGTATAGTTGACAATTCA
H S G K E G S G H G A L L R Y S *
1210
1230
1250
GGACGGTGTGCACTCAAGGTATGCAGCATCACAACCTGACACACGTAGGCATTGTGAAAT
1270
1290
1310
GAGTCCCACAATTGGGCTAATTAACACACCCATCACCTTACATGGTTACTTCTTTCTGTG
1330
1350
1370
GTGAGAACACTAAATTTTAAATAGAGGACACACAGCCTGGGCAACATAGTGAGACCCTGT
1390
1410
1430
CTCTACAAATATAAAAAAATTATCTGGACGTGGTGGTGCACACCTGTGGTCCCAGCTACT
1450
1470
1490
TGGGAAGCTGAGGCTGGAGAATCACTTGAGCCTGGGAGGCGGAGGTTGCGGTGCACTCCA
1510
1530
1550
GCCTGGGCGACAGAGGGAGGCCCTATCTCAAAATAAATAAATAAAGGACACATTCTTATC
1570
AAAAAAAAAAAAAAA

Figure 5C

```
        10                  30                  50
TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG
  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  V

        70                  90                  110
TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG
  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E  R  T  R  V

        130                 150                 170
TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC
  H  E  L  A  T  S  S  A  G  R  D  P  G  S  T  S  C  P  R  P

        190                 210                 230
CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCC
  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  K  G  P  R

        250                 270                 290
GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC
  V  H  E  L  P  T  S  S  P  G  R  D  P  G  S  T  N  C  P  R

        310                 330                 350
GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC
  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  R  G  H

        370                 390                 410
ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC
  R  V  H  E  L  P  T  P  S  P  G  R  D  P  G  F  M  S  C  P

        430                 450                 470
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG
  R  P  L  Q  E  G  T  R  V  H  E  L  P  T  P  S  P  G  G  D

        490                 510                 530
ACCCGGGTCCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCGGGTCCACGAGCTGCC
  P  G  P  R  A  A  H  V  V  N  G  K  G  P  G  S  T  S  C  P
```

Figure 6A

```
      550                 570                 590
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG
  R  P  L  Q  E  G  T  R  V  H  E  L  P  T  R  S  P  G  G  D

      610                 630                 650
ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG
  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A

      670                 690                 710
CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG
  H  V  L  S  R  R  G  H  R  V  H  E  L  P  T  S  S  P  G  G

      730                 750                 770
GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG
  D  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A

      790                 810                 830
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
  A  H  V  L  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E

      850                 870                 890
AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG
  G  T  P  G  S  R  A  A  H  A  L  S  R  K  G  P  R  V  Q  V

      910                 930                 950
TCTCCTGCCGGCCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCCC
  S  C  R  P  T  S  C  L  C  V  N  Q  K  K  D  E  E  Q  A  L

      970                 990                 1010
TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG
  L  S  L  Q  A  G  F  G  G  G  A  G  S  P  A  A  P  S  L  A

      1030                1050                1070
CAGGGCACCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA
  G  H  P  V  L  E  P  Q  N  C  R  R  P  A  E  K  G  S  M  M
```

Figure 6B

```
      1090                1110                1130
TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCCATGGACCTGGATGCCAGTGATGCCTG
  A  P  R  C  A  A  L  D  L  P  P  W  T  W  M  P  V  M  P  E

      1150                1170                1190
AGGTCTGCAGGGCAGTGCATACGCTCACCGCCTGGCCGCTCAGGAGCCTGTGCTTGACCC
  V  C  R  A  V  H  T  L  T  A  W  P  L  R  S  L  C  L  T  P

      1210                1230                1250
CCAAATCCGCCCCCCAACTCCCTGTTACCGGCTCACTCCTTCCATGAGGGGCCTTCCCCA
  K  S  A  P  Q  L  P  V  T  G  S  L  L  P  *

      1270                1290                1310
GGGACAGCCGATGCTCTCCTGATGGCTCCTGCCCTTGCAGAGTGCTGCCCCCGCCTGCCC

      1330                1350                1370
ACCTGGCCTGGACCCTCGCCTGAGCCCCCTCAGGGCTCTGCGCCACCTCAACCCAGGCGT

      1390                1410                1430
TTGTTCCGCAGGAACCTCCCGGCTCTTCCCACTCGGGAAAGGAAGGCTCTGGGCATGGAG

      1450                1470                1490
GTCGGCCAGGCCCCATCCCCGTACCCTGGCCCTTCTTCCTGCTTCCTGTTTGTCACTGCC

      1510                1530                1550
CCGGGGCCTTTGCACCTGCATTCCCTCTCTCTGTGAGTGTCCTGGGGCCCGTTACCCACG

      1570                1590                1610
TCACCGTCCCAGGATACCTTTTCTTTTCTTTCTCTCTCTCCAGCTTTATTGAGGTATAGT

      1630                1650                1670
TGACAATTCAGGACGGTGTGCACTCAAGGTATGCAGCATCACAACCTGACACACGTAGGC

      1690                1710                1730
ATTGTGAAATGAGTCCCACAATTGGGCTAATTAACACACCCATCACCTTACATGGTTACT
```

Figure 6C

```
      1750                1770                1790
      .                   .                   .                   .
TCTTTCTGTGGTGAGAACACTAAATTTTAAATAGAGGACACACAGCCTGGGCAACATAGT

      1810                1830                1850
      .                   .                   .                   .
GAGACCCTGTCTCTACAAATATAAAAAAATTATCTGGACGTGGTGGTGCACACCTGTGGT

      1870                1890                1910
      .                   .                   .                   .
CCCAGCTACTTGGGAAGCTGAGGCTGGAGAATCACTTGAGCCTGGGAGGCGGAGGTTGCG

      1930                1950                1970
      .                   .                   .                   .
GTGCACTCCAGCCTGGGCGACAGAGGGAGGCCCTATCTCAAAATAAATAAATAAAGGACA

      1990                2010
      .                   .                   .
CATTCTTATCAAAAAAAAAAAAAAAAAAA
```

Figure 6D

```
        10                  30                  50
        .                   .                   .
TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG
  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  V

        70                  90                  110
        .                   .                   .
TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG
  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E  R  T  R  V

        130                 150                 170
        .                   .                   .
TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC
  H  E  L  A  T  S  S  A  G  R  D  P  G  S  T  S  C  P  R  P

        190                 210                 230
        .                   .                   .
CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCC
  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  K  G  P  R

        250                 270                 290
        .                   .                   .
GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC
  V  H  E  L  P  T  S  S  P  G  R  D  P  G  S  T  N  C  P  R

        310                 330                 350
        .                   .                   .
GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC
  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  R  G  H

        370                 390                 410
        .                   .                   .
ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC
  R  V  H  E  L  P  T  P  S  P  G  R  D  P  G  F  M  S  C  P

        430                 450                 470
        .                   .                   .
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG
  R  P  L  Q  E  G  T  R  V  H  E  L  P  T  P  S  P  G  G  D

        490                 510                 530
        .                   .                   .
ACCCGGGTCCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCGGGTCCACGAGCTGCC
  P  G  P  R  A  A  H  V  V  N  G  K  G  P  G  S  T  S  C  P
```

Figure 7A

```
      550                 570                 590
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG
  R  P  L  Q  E  G  T  R  V  H  E  L  P  T  R  S  P  G  G  D

      610                 630                 650
ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG
  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A

      670                 690                 710
CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG
  H  V  L  S  R  R  G  H  R  V  H  E  L  P  T  S  S  P  G  G

      730                 750                 770
GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG
  D  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A

      790                 810                 830
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
  A  H  V  L  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E

      850                 870                 890
AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG
  G  T  P  G  S  R  A  A  H  A  L  S  R  K  G  P  R  V  Q  V

      910                 930                 950
TCTCCTGCCGGCCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCCC
  S  C  R  P  T  S  C  L  C  V  N  Q  K  K  D  E  E  Q  A  L

      970                 990                 1010
TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG
  L  S  L  Q  A  G  F  G  G  G  A  G  S  P  A  A  P  S  L  A

      1030                1050                1070
CAGGGCACCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA
  G  H  P  V  L  E  P  Q  N  C  R  R  P  A  E  K  G  S  M  M
```

Figure 7B

```
      1090                1110                1130
TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCCATGGACCTGGGAACCTCCCGGCTCTT
  A  P  R  C  A  A  L  D  L  P  P  W  T  W  E  P  P  G  S  S

      1150                1170                1190
CCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGGTCGGCCAGGCCCCATCCCCGTACCCT
  H  S  G  K  E  G  S  G  H  G  G  R  P  G  P  I  P  V  P  W

      1210                1230                1250
GGCCCTTCTTCCTGCTTCCTGTTTGTCACTGCCCCGGGGCCTTTGCACCTGCATTCCCTC
  P  F  F  L  L  P  V  C  H  C  P  G  A  F  A  P  A  F  P  L

      1270                1290                1310
TCTCTGTGAGTGTCCTGGGGCCCGTTACCCACGTCACCGTCCCAGGATACCTTTTCTTTT
  S  V  S  V  L  G  P  V  T  H  V  T  V  P  G  Y  L  F  F  S

      1330                1350                1370
CTTTCTCTCTCTCCAGCTTTATTGAGGTATAGTTGACAATTCAGGACGGTGTGCACTCAA
  F  S  L  S  S  F  I  E  V  *

      1390                1410                1430
GGTATGCAGCATCACAACCTGACACACGTAGGCATTGTGAAATGAGTCCCACAATTGGGC

      1450                1470                1490
TAATTAACACACCCATCACCTTACATGGTTACTTCTTTCTGTGGTGAGAACACTAAATTT

      1510                1530                1550
TAAATAGAGGACACACAGCCTGGGCAACATAGTGAGACCCTGTCTCTACAAATATAAAAA

      1570                1590                1610
AATTATCTGGACGTGGTGGTGCACACCTGTGGTCCCAGCTACTTGGGAAGCTGAGGCTGG

      1630                1650                1670
AGAATCACTTGAGCCTGGGAGGCGGAGGTTGCGGTGCACTCCAGCCTGGGCGACAGAGGG
```

Figure 7C

1690 1710 1730

AGGCCCTATCTCAAAATAAATAAATAAAGGACACATTCTTATCAAAAAAAAAAAAAAAAA

AAAA

Figure 7D

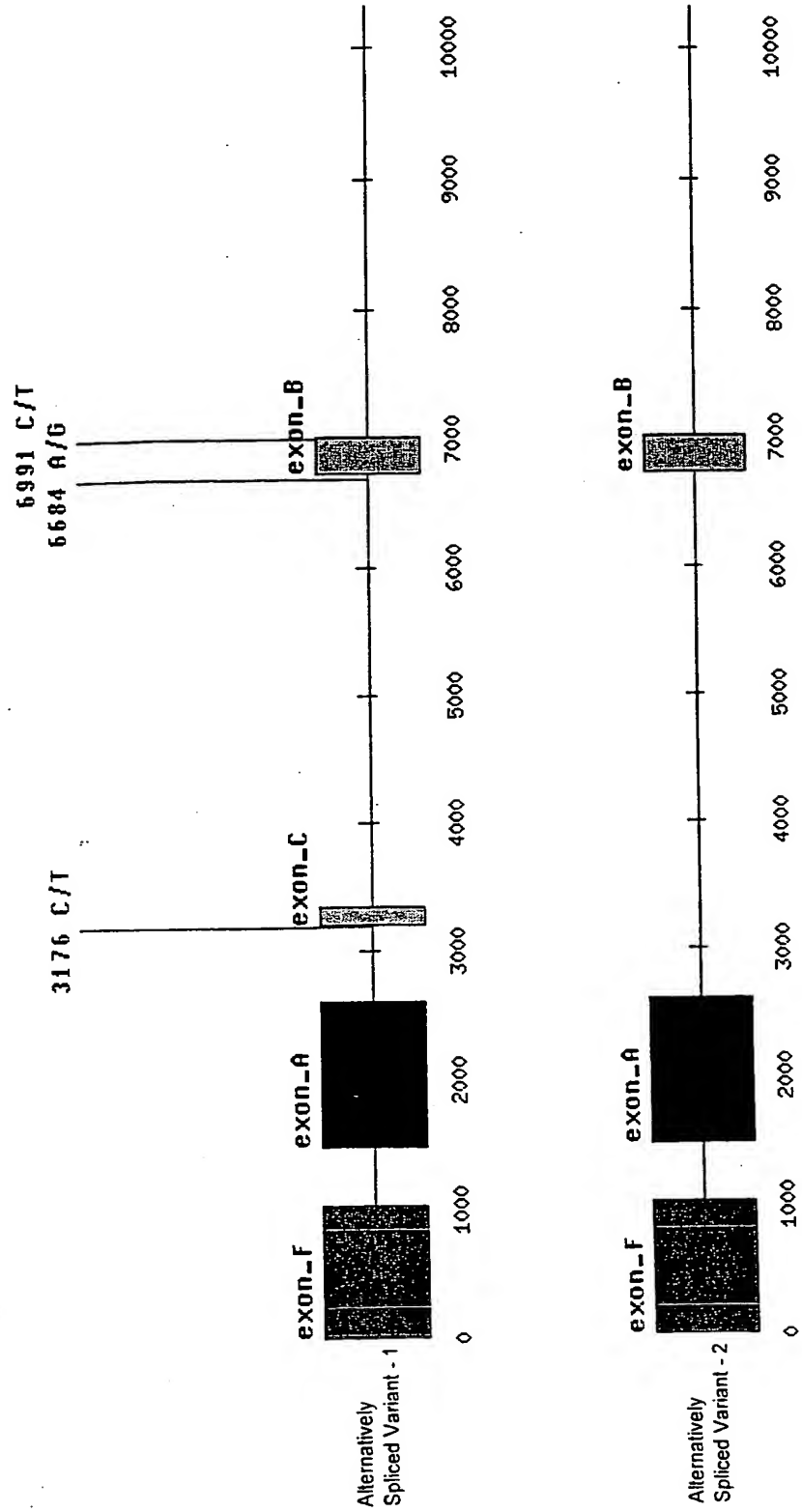
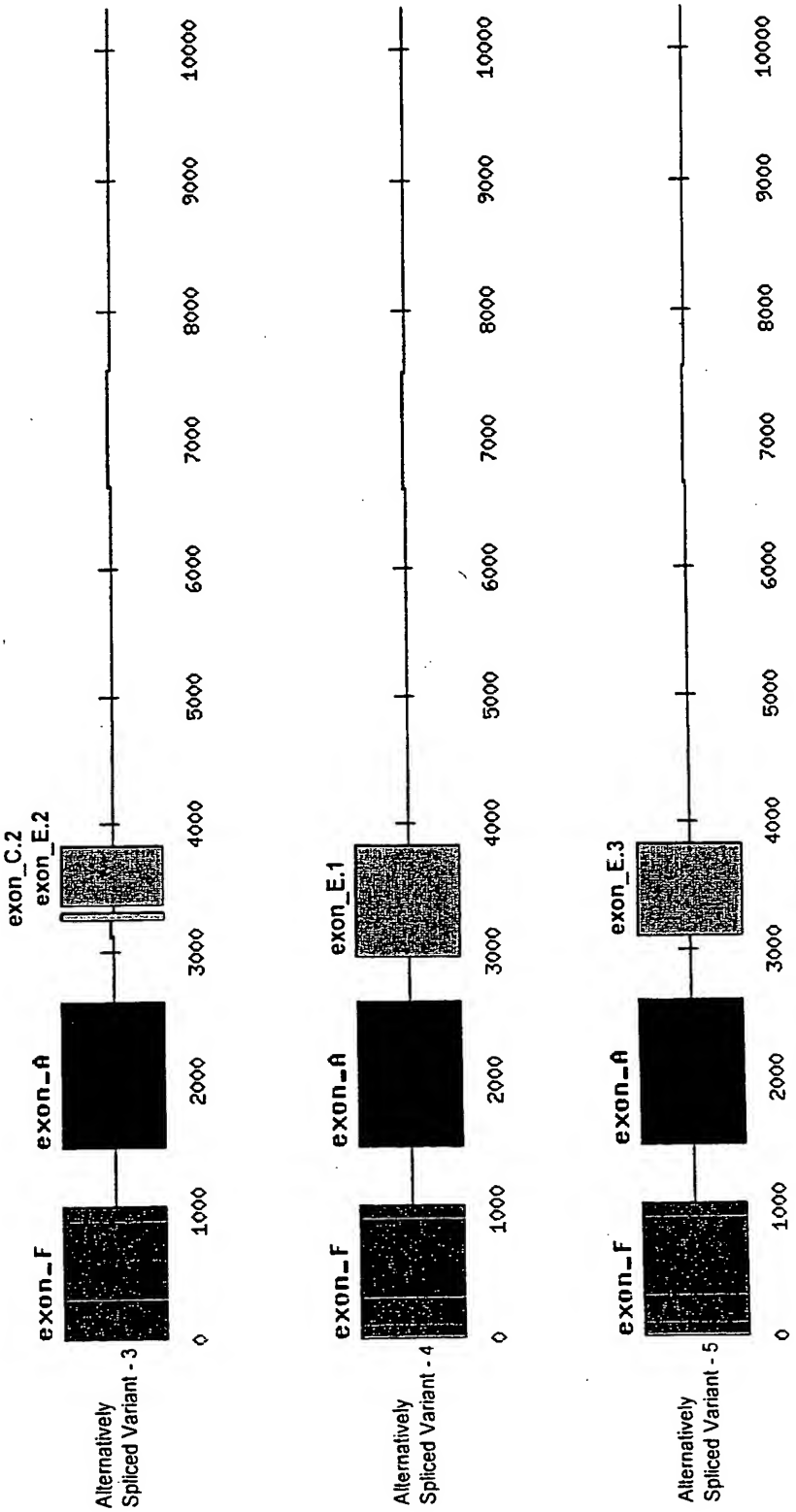

Alternatively Spliced Variants from Gene 214
Alternatively Spliced Variant - 1
Alternatively Spliced Variant - 2
exon_F
exon_A
exon_C
exon_B
3176 C/T
6684 A/G
6991 C/T
0
1000
2000
3000
4000
5000
6000
7000
8000
9000
10000

Figure 8A



Alternatively Spliced Variants from Gene 214

Figure 8B

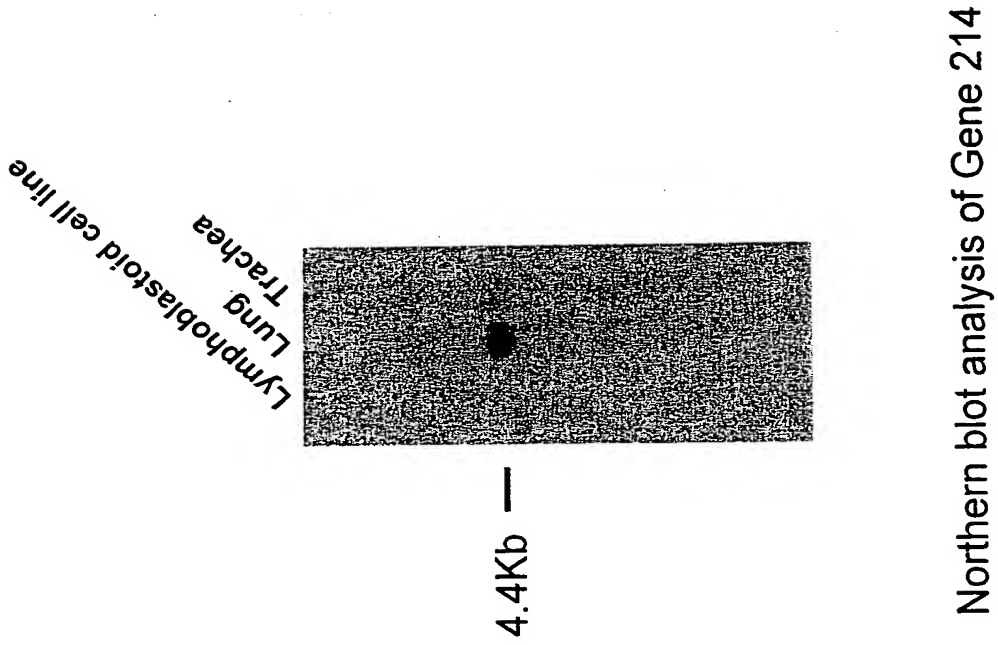

Northern blot analysis of Gene 214
4.4Kb
Lymphoblastoid cell line
Lung
Trachea

Figure 9

>Gene 214 Exon_A
TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG
TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG
TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC
CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCC
GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC
GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC
ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG
ACCCGGGTCCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCGGGTCCACGAGCTGCC
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG
ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG
CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG
GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG
TCTCCTGCCGGCCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCCC
TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG
CAGGGCACCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA
TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCCATGGACCTGG

>Gene 214 Exon_B
AGACAGGGTTTCTCCTCATTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGACGATCCAC
CTGCCTCAGCCTCCCGAAGTGTTGGGATTACAGGCACGAGCCACTGTGCCCGGCCATCAT
TCCTTTTTACTGCTGACTAATAGTCTGCTGTGTGAATCCACCGCTAGAAACCCACTCATC
AGTTGATGGTCATGTGGGTTGCTTCTGCTATTCGCTTATTATGAACAGTGCTGGAATAAA
CGTTCCTGTGCACTCTTGGGCATACGCCTAGGAGTGGAACTGCTGGGTC

>Gene 214 Exon C
GAACCTCCCGGCTCTTCCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGGTCGGCCAGGC
CCCATCCCCGTACCCTGGCCCTTCTTCCTGCTTCCTGTTTGTCACTGCCCCGGGGCCTTT
GCACCTGCATTCCCTCTCTCT

>Gene 214 Exon C.2
GAACCTCCCGGCTCTTCCCACTCGGGAAAGGAAGGCTCTGGGCATGGAG

>Gene 214 Exon E.1
ATGCCAGTGATGCCTGAGGTCTGCAGGGCAGTGCATACGCTCACCGCCTGGCCGCTCAGG
AGCCTGTGCTTGACCCCCAAATCCGCCCCCCAACTCCCTGTTACCGGCTCACTCCTTCCA
TGAGGGGCCTTCCCCAGGGACAGCCGATGCTCTCCTGATGGCTCCTGCCCTTGCAGAGTG
CTGCCCCCGCCTGCCCACCTGGCCTGGACCCTCGCCTGAGCCCCCTCAGGGCTCTGCGCC
ACCTCAACCCAGGCGTTTGTTCCGCAGGAACCTCCCGGCTCTTCCCACTCGGGAAAGGAA
GGCTCTGGGCATGGAGGTCGGCCAGGCCCCATCCCCGTACCCTGGCCCTTCTTCCTGCTT
CCTGTTTGTCACTGCCCCGGGGCCTTTGCACCTGCATTCCCTCTCTCTGTGAGTGTCCTG
GGGCCCGTTACCCACGTCACCGTCCCAGGATACCTTTTCTTTTCTTTCTCTCTCTCCAGC
TTTATTGAGGTATAGTTGACAATTCAGGACGGTGTGCACTCAAGGTATGCAGCATCACAA
CCTGACACACGTAGGCATTGTGAAATGAGTCCCACAATTGGGCTAATTAACACACCCATC
ACCTTACATGGTTACTTCTTTCTGTGGTGAGAACACTAAATTTTAAATAGAGGACACACA
GCCTGGGCAACATAGTGAGACCCTGTCTCTACAAATATAAAAAAATTATCTGGACGTGGT
GGTGCACACCTGTGGTCCCAGCTACTTGGGAAGCTGAGGCTGGAGAATCACTTGAGCCTG
GGAGGCGGAGGTTGCGGTGCACTCCAGCCTGGGCGACAGAGGGAGGCCCTATCTCAAAAT
AAATAAATAAAGGACACATTCTTATC

FIGURE 10A

>Gene 214 Exon E.2
CTTTATTGAGGTATAGTTGACAATTCAGGACGGTGTGCACTCAAGGTATGCAGCATCACA
ACCTGACACACGTAGGCATTGTGAAATGAGTCCCACAATTGGGCTAATTAACACACCCAT
CACCTTACATGGTTACTTCTTTCTGTGGTGAGAACACTAAATTTTAAATAGAGGACACAC
AGCCTGGGCAACATAGTGAGACCCTGTCTCTACAAATATAAAAAAATTATCTGGACGTGG
TGGTGCACACCTGTGGTCCCAGCTACTTGGGAAGCTGAGGCTGGAGAATCACTTGAGCCT
GGGAGGCGGAGGTTGCGGTGCACTCCAGCCTGGGCGACAGAGGGAGGCCCTATCTCAAAA
TAAATAAATAAAGGACACATTCTTATC

>Gene 214 Exon E.3
GAACCTCCCGGCTCTTCCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGGTCGGCCAGGC
CCCATCCCCGTACCCTGGCCCTTCTTCCTGCTTCCTGTTTGTCACTGCCCCGGGGCCTTT
GCACCTGCATTCCCTCTCTCTGTGAGTGTCCTGGGGCCCGTTACCCACGTCACCGTCCCA
GGATACCTTTTCTTTTCTTTCTCTCTCTCCAGCTTTATTGAGGTATAGTTGACAATTCAG
GACGGTGTGCACTCAAGGTATGCAGCATCACAACCTGACACACGTAGGCATTGTGAAATG
AGTCCCACAATTGGGCTAATTAACACACCCATCACCTTACATGGTTACTTCTTTCTGTGG
TGAGAACACTAAATTTTAAATAGAGGACACACAGCCTGGGCAACATAGTGAGACCCTGTC
TCTACAAATATAAAAAAATTATCTGGACGTGGTGGTGCACACCTGTGGTCCCAGCTACTT
GGGAAGCTGAGGCTGGAGAATCACTTGAGCCTGGGAGGCGGAGGTTGCGGTGCACTCCAG
CCTGGGCGACAGAGGGAGGCCCTATCTCAAAATAAATAAATAAAGGACACATTCTTATC

>Gene 214 Exon F
CGGGCGTGTATATCTCTTCATAGAGAGCGCTCAGACAGCGTGCGTTAATCTGCGTCGATA
TATAGAGATCTTTATCACTGAGTAGATAGAACGTACATGAATGTACGAACAGTCCAGACG
AGTAACTTGACTAGGATAAGATAGACAGTACCAACTAATGAGACAAGAAGAGGGAATCAT
ATAGAATCATGTAGTCTGAGTCTAGCGAGTGTCGACATGATCACAAGCGAAATACAGACT
ATGAGAAGAGGTAGAAATAATAAGTANACTGAGAAGAGAGGTCATATGTACATACAAATC
AGTAAAGCAATAGAAATTGAATACATTATAAGCCACAGTTACAGAATTAGCCTAATTTAA
CAACCATGGCAAGCGAGTTATATCAAACATAGAAGAGTAAACTCTATCGACCATGGGTAG
GAACGAATAAAGGCGTCGAGAAGACAATAAGAATGCGTGTTAAACAGCAATACAAGAGAA
TAGCACCACTGAAGCAGACCAAAGGCGTCACCGGGGAAGTAGGGAAGAGGCACCTCACAA
GGAGAGGAAAGGGCAGTCCTGATTTTGAAAATTTCAGTGAAAAGACAGTGTTGTTCCCGG
AGGCAGCTTAGTGATCCCGCATCGACTCTGAAGAGGACCCTGAGGGTAGGGGATTTTTGG
GCCTGACCGGCCTATGCTGAACGCCCACCGGGAATTCAGGGAGAAACACGGGGCCCCGGC
TTCCAGGAGAGCAGCCAGGCCACAGCCCTGAGGACGGGCAAACCCCACCCAGGCACGGTG
AGAGGGAGGCCGCCCAGGCCTGGGGCCTGGCGGCAGGGGATGAAGTGGACCAGAGCCCCG
CAAATCCTAACGTGGGTGAGCAGTGAGCCTGTGTGGCTGCGAGTGGCTCCGTTTTGGGGC
TGTTTGTTCCTGCAGCAAATGATGCCAGCCCTGACGGAACCAGTGCACGTCCACCACGAG
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
AAGGGACC

FIGURE 10B